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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/425,804	10/25/1999	DAVID G. GORENSTEIN	122144-1001	1041

7590 12/06/2001

Gardere Wynne Sewell LLP
Sanford E. Warren, Jr.
3000 Thanksgiving Tower
1601 Elm Street
DALLAS, TX 75201-4761

EXAMINER

BHATTI, TAHIRA H

ART UNIT	PAPER NUMBER
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1627

12

DATE MAILED: 12/06/2001

Please find below and/or attached an Office communication concerning this application or proceeding.

file
copy



UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office
COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/425,804			

EXAMINER	
ART UNIT	PAPER NUMBER
1627	12

Please find below a communication from the EXAMINER in charge of this application

Sequence Rules: Bonafide Attempt Letter

The forwarded Sequence Letter e.g. "Notice to Comply with Sequence Rules" dated 10/1/01 in paper no. 10 is hereby vacated in light of the "Raw Sequence Listing Error Report" received by the Examiner on 10/5/01 (paper no. 11) a copy of which is enclosed herewith.

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2); but fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth on the attached "Raw Sequence Listing Error Report". Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be further examined.

Since the above-mentioned reply appears to be *bona fide* attempt to comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825), applicant is given a TIME PERIOD of **ONE (1) MONTH** from the mailing date of this communication within which to correct the deficiency so as to comply with the sequence rules (37 CFR 1.821 - 1.825) in order to avoid abandonment of the application under 37 CFR 1.821(g). EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).

General information regarding further correspondence

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Examiner Celsa whose telephone number is (703) 305-7556.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Jyothsna Venkat (art unit 1627), can be reached at (703)308-0570.

Any inquiry of a general nature, or relating to the status of this application, should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Tahira Bhatti (art unit 1627)

December 3, 2001

BENNETT CELSA
PRIMARY EXAMINER

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(d).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached marked-up copy of the "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).
- ☐ 7. Other: _____

Applicant must provide:

- ☒ An ~~initial~~ or substitute computer readable form (CRF) copy of the "Sequence Listing"
- ☒ An ~~initial~~ or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123
 For CRF submission help, call (703) 308-4212
 For Patent/In software help, call (703) 308-6856

Please return a copy of this notice with your response.

PRFV

BIOTECHNOLOGY
SYSTEMS
BRANCH



11
M.M.
10/19/01

**RAW SEQUENCE LISTING
ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/425,804

Source: 1623

Date Processed by STIC: 9/27/2001

RECEIVED

OCT 05 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OCT 05 2001

TECH CENTER 1600/2900

Raw Sequence Listing Error Summary

ERROR DETECTED**SUGGESTED CORRECTION**

SERIAL NUMBER: 09/425,804.

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

1623

RAW SEQUENCE LISTING

DATE: 09/27/2001

PATENT APPLICATION: US/09/425,804

TIME: 11:23:40

Input Set : A:\Nfkbapt1.app

Output Set: N:\CRF3\09272001\I425804.raw

3 <110> APPLICANT: Gorenstein, David G.
 4 King, David J.
 5 Ventura, Daniel A.
 6 Brasier, Allan R.
 8 <120> TITLE OF INVENTION: Thio-Modified Aptamer Synthetic Methods and
 9 Compositions
 11 <130> FILE REFERENCE: 122144-002000
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/425,804
 C--> 14 <141> CURRENT FILING DATE: 1999-10-25
 16 <150> PRIOR APPLICATION NUMBER: 60/105,600
 17 <151> PRIOR FILING DATE: 1998-10-26
 19 <160> NUMBER OF SEQ ID NOS: 50
 21 <170> SOFTWARE: PatentIn Ver. 2.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 66
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Artificial Sequence
 28 <220> FEATURE:
 29 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
 31 <400> SEQUENCE: 1
 W--> 32 cagtgtctta gaggatccgt gacnnnnnnn nnnnnnnnnn nnnnnn-gaag cttatcgatc 60
 33 cgagcg 66
 36 <210> SEQ ID NO: 2
 37 <211> LENGTH: 22
 38 <212> TYPE: DNA
 39 <213> ORGANISM: Artificial Sequence
 41 <220> FEATURE:
 42 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
 44 <400> SEQUENCE: 2
 45 gccgtccaca tacgacacca cc 22
 48 <210> SEQ ID NO: 3
 49 <211> LENGTH: 22
 50 <212> TYPE: DNA
 51 <213> ORGANISM: Artificial Sequence
 53 <220> FEATURE:
 54 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
 56 <400> SEQUENCE: 3
 57 ggccgaccgc acagcacaac cc 22
 60 <210> SEQ ID NO: 4
 61 <211> LENGTH: 22
 62 <212> TYPE: DNA
 63 <213> ORGANISM: Artificial Sequence
 65 <220> FEATURE:
 66 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
 68 <400> SEQUENCE: 4
 69 ggcgcggata caaccacac gc 22
 72 <210> SEQ ID NO: 5

Does Not Comply
 Corrected Diskette Needed

See item # 9 on
 Error summary
 sheet.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/425,804

DATE: 09/27/2001

TIME: 11:23:40

Input Set: A:\Nfkbapt1.app

Output Set: N:\CRF3\09272001\I425804.raw

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73 <211> LENGTH: 22
74 <212> TYPE: DNA
75 <213> ORGANISM: Artificial Sequence
77 <220> FEATURE:
78 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
80 <400> SEQUENCE: 5
81 gggcccgcgtg tacatgcaca cg 22
84 <210> SEQ ID NO: 6
85 <211> LENGTH: 22
86 <212> TYPE: DNA
87 <213> ORGANISM: Artificial Sequence
89 <220> FEATURE:
90 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
92 <400> SEQUENCE: 6
93 ggccgaccgc acagcacaac cc 22
96 <210> SEQ ID NO: 7
97 <211> LENGTH: 22
98 <212> TYPE: DNA
99 <213> ORGANISM: Artificial Sequence
101 <220> FEATURE:
102 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
104 <400> SEQUENCE: 7
105 gggcccgcgtg tacatgcaca cg 22
108 <210> SEQ ID NO: 8
109 <211> LENGTH: 22
110 <212> TYPE: DNA
111 <213> ORGANISM: Artificial Sequence
113 <220> FEATURE:
114 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
116 <400> SEQUENCE: 8
117 gggcccgcgtg cacgtgcaca cg 22
120 <210> SEQ ID NO: 9
121 <211> LENGTH: 22
122 <212> TYPE: DNA
123 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
128 <400> SEQUENCE: 9
129 gggcccgcgtg tacacgcaca cg 22
132 <210> SEQ ID NO: 10
133 <211> LENGTH: 22
134 <212> TYPE: DNA
135 <213> ORGANISM: Artificial Sequence
137 <220> FEATURE:
138 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
140 <400> SEQUENCE: 10
141 cccgttggtg tcccactcca cg 22
144 <210> SEQ ID NO: 11
145 <211> LENGTH: 22

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RAW SEQUENCE LISTING

DATE: 09/27/2001

PATENT APPLICATION: US/09/425,804

TIME: 11:23:40

Input Set : A:\Nfkbapt1.app

Output Set: N:\CRF3\09272001\I425804.raw

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146 <212> TYPE: DNA
147 <213> ORGANISM: Artificial Sequence
149 <220> FEATURE:
150 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
152 <400> SEQUENCE: 11
153 cccgttggtg tcccgtcca cg 22
156 <210> SEQ ID NO: 12
157 <211> LENGTH: 10
158 <212> TYPE: DNA
159 <213> ORGANISM: Artificial Sequence
161 <220> FEATURE:
162 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
164 <400> SEQUENCE: 12
165 gttgcgcaac 10
168 <210> SEQ ID NO: 13
169 <211> LENGTH: 10
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
176 <400> SEQUENCE: 13
177 gctgtacatg 10
180 <210> SEQ ID NO: 14
181 <211> LENGTH: 10
182 <212> TYPE: DNA
183 <213> ORGANISM: Artificial Sequence
185 <220> FEATURE:
186 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
188 <400> SEQUENCE: 14
189 gttgtccac 10
192 <210> SEQ ID NO: 15
193 <211> LENGTH: 10
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
200 <400> SEQUENCE: 15
201 gttgttgtcc 10
204 <210> SEQ ID NO: 16
205 <211> LENGTH: 20
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
209 <220> FEATURE:
210 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
212 <400> SEQUENCE: 16
213 tgcagattgc gcaatctgca 20
216 <210> SEQ ID NO: 17
217 <211> LENGTH: 22
218 <212> TYPE: DNA

```

RAW SEQUENCE LISTING

DATE: 09/27/2001

PATENT APPLICATION: US/09/425,804

TIME: 11:23:40

Input Set : A:\Nfkbaptl.app

Output Set: N:\CRF3\09272001\I425804.raw

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219 <213> ORGANISM: Artificial Sequence
221 <220> FEATURE:
222 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
224 <400> SEQUENCE: 17
225 cgtgtgcatg tacagcgggc cc 22
228 <210> SEQ ID NO: 18
229 <211> LENGTH: 42
230 <212> TYPE: DNA
231 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
234 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
236 <400> SEQUENCE: 18
237 ccaggagatt ccaccagga gattccaccc aggagattcc ac 42
240 <210> SEQ ID NO: 19
241 <211> LENGTH: 14
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
248 <400> SEQUENCE: 19
249 ccaggagatt ccac 14
252 <210> SEQ ID NO: 20
253 <211> LENGTH: 10
254 <212> TYPE: DNA
255 <213> ORGANISM: Artificial Sequence
257 <220> FEATURE:
258 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
260 <400> SEQUENCE: 20
261 ggggacttcc 10
264 <210> SEQ ID NO: 21
265 <211> LENGTH: 62
266 <212> TYPE: DNA
267 <213> ORGANISM: Artificial Sequence
269 <220> FEATURE:
270 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
272 <400> SEQUENCE: 21
W--> 273 atgcttcac ggcctttt nnnnnnnnnn nnnnnnnnnn nctgcgaggc ggtagtctat 60
274 tc 62
277 <210> SEQ ID NO: 22
278 <211> LENGTH: 22
279 <212> TYPE: DNA
280 <213> ORGANISM: Artificial Sequence
282 <220> FEATURE:
283 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
285 <400> SEQUENCE: 22
286 ggggcggggg gatatggaca cc 22
289 <210> SEQ ID NO: 23
290 <211> LENGTH: 22
291 <212> TYPE: DNA

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see page 1

RAW SEQUENCE LISTING

DATE: 09/27/2001

PATENT APPLICATION: US/09/425,804

TIME: 11:23:40

Input Set : A:\Nfkbapt1.app

Output Set: N:\CRF3\09272001\I425804.raw

292 <213> ORGANISM: Artificial Sequence
 294 <220> FEATURE:
 295 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
 297 <400> SEQUENCE: 23
 298 gggctggtgt ggtagactcc cc 22
 301 <210> SEQ ID NO: 24
 302 <211> LENGTH: 22
 303 <212> TYPE: DNA
 304 <213> ORGANISM: Artificial Sequence
 306 <220> FEATURE:
 307 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
 309 <400> SEQUENCE: 24
 310 cccgcccaca cacaccgccc cc 22
 313 <210> SEQ ID NO: 25
 314 <211> LENGTH: 23
 315 <212> TYPE: DNA
 316 <213> ORGANISM: Artificial Sequence
 318 <220> FEATURE:
 319 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
 321 <400> SEQUENCE: 25
 322 gggccgggag agaacatagc gac 23
 325 <210> SEQ ID NO: 26
 326 <211> LENGTH: 22
 327 <212> TYPE: DNA
 328 <213> ORGANISM: Artificial Sequence
 330 <220> FEATURE:
 331 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
 333 <400> SEQUENCE: 26
 W--> 334 cccnnnnca cacaccgccc cc 22 *see page 1*
 337 <210> SEQ ID NO: 27
 338 <211> LENGTH: 22
 339 <212> TYPE: DNA
 340 <213> ORGANISM: Artificial Sequence
 342 <220> FEATURE:
 343 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
 345 <400> SEQUENCE: 27
 346 ggtatactct ccgcccctcc cc 22
 349 <210> SEQ ID NO: 28
 350 <211> LENGTH: 26
 351 <212> TYPE: DNA
 352 <213> ORGANISM: Artificial Sequence
 354 <220> FEATURE:
 355 <223> OTHER INFORMATION: Description of Artificial Sequence: aptamer
 357 <400> SEQUENCE: 28
 358 cccacatgta cagccgccc ccgccc 26
 361 <210> SEQ ID NO: 29
 362 <211> LENGTH: 22
 363 <212> TYPE: DNA
 364 <213> ORGANISM: Artificial Sequence

FYI!
 Use of n and Y or Xaa has been detected in the
 Sequence Listing. Review the Sequence Listing
 to ensure a corresponding explanation is present
 in the <220> to <223> fields of each sequence
 using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/425,804

DATE: 09/27/2001

TIME: 11:23:41

Input Set : A:\Nfkbapt1.app

Output Set: N:\CRF3\09272001\I425804.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:32 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:32 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:32 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:273 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:273 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:334 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
L:334 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26
L:334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:370 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29
L:370 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:29
L:370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29